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Om protein - protein search, using sw model.

Run on:

December 30, 2002, 16:17:08 ; Search time 10 Seconds

(without alignments)

112.542 Million cell. updates/sec

title:

US-09-664-326-23

Perfect score:

368

Sequence:

1 LTYDCTESQNLCLCEGSN.....PKPQSHNDGFEEIPEEYLQ 65

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

109717 seqs, 17314136 residues

Total number of hits satisfying chosen parameters:

109717

Minimum DB seq length:

0

Maximum DB seq length:

200000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubbeta/us08_NEWW_PUB_pep:*

2: /cgn2_6/ptodata/1/pubbeta/pctc_NEWW_PUB_pep:*

3: /cgn2_6/ptodata/1/pubbeta/us06_NEWW_PUB_pep:*

4: /cgn2_6/ptodata/1/pubbeta/us06_PUBCOMB_pep:*

5: /cgn2_6/ptodata/1/pubbeta/us07_NEWW_PUB_pep:*

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13: /cgn2_6/ptodata/1/pubbeta/us60_NEWW_PUB_pep:*

14: /cgn2_6/ptodata/1/pubbeta/us60_PUBCOMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description
1	368	100.0	65	9	US-09-899-235-15
2	113.5	100.0	73	10	US-09-779-054-12
3	77	20.9	14	10	US-09-765-61AB-29
4	77	20.9	14	10	US-09-925-71B-25
5	77	20.9	15	10	US-09-765-61AB-18
6	77	20.9	15	10	US-09-925-71B-18
7	70	19.0	160	10	US-09-798-042-100
8	70	19.0	323	10	US-09-798-042-9
9	70	19.0	658	10	US-09-798-042-85
10	70	19.0	658	10	US-09-798-042-93
11	70	19.0	315	9	US-09-809-602-65
12	69	18.8	1218	10	US-09-855-722-7
13	68.5	18.6	323	9	US-09-976-165-34
14	66.5	18.1	810	10	US-09-976-165-34
15	66	17.9	197	12	US-10-000-916-6
16	64	17.4	18	10	US-09-905-831-5
17	64	17.4	51	12	US-10-000-252A-75
18	64	17.4	379	10	US-09-864-761-4322
19	63.5	17.3	568	10	US-09-945-676-7

ALIGNMENTS

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US-09-899-235-15

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; Best Local Similarity 100.0%; Score 368; DB 9; Length 65;

Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 EEEYLQ 65

RESULT 2

US-09-779-054-12

; Sequence 12, Application US/0979054

; Patent No. US20030120102A1

; GENERAL INFORMATION:

; APPLICANT: Lu, Xinjie

; APPLICANT: Kakkar, Vijay

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 ; CURRENT APPLICATION NUMBER: US/09/779, 054
 ; CURRENT FILING DATE: 2001-02-05
 ; PRIORITY FILING DATE: 2000-02-05
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn version 3.0
 ; LENGTH: 73
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Modified dendroaspin (KGDM-dendroaspin-Hr)
 ; US-09-779-054-12

Query Match 30.9%; Score 113.5; DB 10; Length 73;
 Best Local Similarity 64.7%; Pred. No. 9.5e-06;
 Matches 22; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

Qy 39 CIVGEGST-----PKPQSHNDGFEEIPEEYLAQ 65
 Db 40 CFTPKGDMPGPYCPRPQSHNDGFEEIPEEYLAQ 73

RESULT 3
 US-09-765-614B-29
 ; Sequence 29, Application US/09765614B
 ; Patent No. US20020102215A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nycomed Imaging AS
 ; TITLE OF INVENTION: Improvements in or relating to
 ; TITLE OF INVENTION: diagnostic/therapeutic
 ; TITLE OF INVENTION: agents
 ; FILE REFERENCE: REFKlavennes/054
 ; CURRENT APPLICATION NUMBER: US/09/765, 614B
 ; CURRENT FILING DATE: 2001-07-10
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 29
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial
 ; OTHER INFORMATION: Sequence:Thrombus
 ; OTHER INFORMATION: binding peptide
 ; US-09-765-614B-29

Query Match 20.9%; Score 77; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 NDGDFEEIPEEYLAQ 65
 Db 1 NDGDFEEIPEEYLAQ 14

RESULT 4
 US-09-925-715-25
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 ; Patent No. US20020102217A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nycomed Imaging AS
 ; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
 ; TITLE OF INVENTION: agents
 ; FILE REFERENCE: REFKlavennes/206
 ; CURRENT APPLICATION NUMBER: US/09/925, 715
 ; CURRENT FILING DATE: 2001-08-10
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: binding peptide
 ; US-09-925-715-25

Query Match 20.9%; Score 77; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 NDGDFEEIPEEYLAQ 65
 Db 2 NDGDFEEIPEEYLAQ 15

RESULT 5
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 ; Sequence 18, Application US/09765614B
 ; Patent No. US20020102215A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nycomed Imaging AS
 ; TITLE OF INVENTION: Improvements in or relating to
 ; TITLE OF INVENTION: diagnostic/therapeutic
 ; TITLE OF INVENTION: agents
 ; FILE REFERENCE: REFKlavennes/054
 ; CURRENT APPLICATION NUMBER: US/09/765, 614B
 ; CURRENT FILING DATE: 2001-07-10
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial
 ; OTHER INFORMATION: Sequence:Lipopeptide
 ; OTHER INFORMATION: with affinity for thrombi
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)
 ; OTHER INFORMATION: Dipalmitoyl-Lys
 ; NAME/KEY: MOD_RES
 ; LOCATION: (15)
 ; OTHER INFORMATION: (15)
 ; OTHER INFORMATION: AMIDATION
 ; US-09-765-614B-18

Query Match 20.9%; Score 77; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 NDGDFEEIPEEYLAQ 65
 Db 2 NDGDFEEIPEEYLAQ 15

RESULT 6
 US-09-925-715-18
 ; Sequence 18, Application US/09925715
 ; Patent No. US20020102217A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nycomed Imaging AS
 ; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
 ; TITLE OF INVENTION: agents
 ; FILE REFERENCE: REFKlavennes/206
 ; CURRENT APPLICATION NUMBER: US/09/925, 715
 ; CURRENT FILING DATE: 2001-08-10
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:Lipopptide
 OTHER INFORMATION: with an affinity for thrombi
 NAME/KEY: MOD-RES
 LOCATION: (1)
 OTHER INFORMATION: Dipalmitoyl-lysine

NAME/KEY: MOD-RES
 LOCATION: (15)
 OTHER INFORMATION: AMIDATION

US-09-925-715-18

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 Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 52 NDDDFERIPEEYLQ 65
 Db 2 NDDFEEFEEVEYLQ 15

RESULT 7

US-09-798-042-100

Sequence 100, Application US/09798042

Patent No. US20020068343A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

FILE REFERENCE: 210121.439C7

CURRENT APPLICATION NUMBER: US/09/798,042

CURRENT FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 108

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 100

LENGTH: 160

TYPE: PRT

ORGANISM: *Ehrlichia* sp.

US-09-798-042-100

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 Db 79 CGDNGSSSTTTSGTNSETGQVERDFIRATLKEKGSKNWPSSGTGIPKPVINDAKAVA 138

QY 57 -----EEIPEE 62
 Db 139 KDLVQELTPEE 149

RESULT 8

US-09-159-469-9

Sequence 9, Application US/09159469

Patent No. US2002004535A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

FILE REFERENCE: 210121.439C7

CURRENT APPLICATION NUMBER: US/09/798,042

CURRENT FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 108

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 9

LENGTH: 323

TYPE: PRT

ORGANISM: *Ehrlichia* sp.

US-09-798-042-9

Query Match 19.0%; Score 70; DB 10; Length 323;
 Best Local Similarity 29.6%; Pred. No. 1.9; Mismatches 21; Conservative 10; Indels 14; Gaps 3;

Matches 21; Conservative 10; Indels 14; Gaps 3;

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

FILE REFERENCE: 210121.439C7

CURRENT APPLICATION NUMBER: US/09/798,042

CURRENT FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 108

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 9

LENGTH: 323

TYPE: PRT

ORGANISM: *Ehrlichia* sp.

US-09-798-042-9

Query Match 19.0%; Score 70; DB 10; Length 323;
 Best Local Similarity 29.6%; Pred. No. 1.9; Mismatches 21; Conservative 10; Indels 14; Gaps 3;

Matches 21; Conservative 10; Indels 14; Gaps 3;

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

FILE REFERENCE: 210121.439C7

CURRENT APPLICATION NUMBER: US/09/798,042

CURRENT FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 108

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 9

LENGTH: 323

TYPE: PRT

ORGANISM: *Ehrlichia* sp.

US-09-798-042-9

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/159,469
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/106,582
 FILING DATE: 29-JUN-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.439C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-622-4900
 TELEFAX: 206-622-6031

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 323 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 323 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein

Query Match 19.0%; Score 70; DB 10; Length 323;
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 Matches 21; Conservative 10; Indels 14; Gaps 3;

QY 6 CTESGQNCLCCEGSNVCGQGN-----KCILGSDGEKN-QCVTGEGPKPQSHNDGDF-- 56
 Db 185 CGDNGSSSTTTSGTNSETGQVERDFIRATLKEKGSKNWPSSGTGIPKPVINDAKAVA 244

QY 57 -----EEIPEE 62

Db 245 KDLVQELTPEE 255

Query Match 19.0%; Score 70; DB 10; Length 323;
 Best Local Similarity 29.6%; Pred. No. 1.9; Mismatches 21; Conservative 10; Indels 14; Gaps 3;
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QY 57 -----EEIPEE 62

Db 245 KDLVQELTPEE 255

RESULT 10
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 ; Sequence 85, Application US/09798042
 ; Patent No. US2002068343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; Lodes, Michael J.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 ; FILE REFERENCE: 210121.439C7
 ; CURRENT APPLICATION NUMBER: US/09/798, 042
 ; CURRENT FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 85
 ; LENGTH: 658
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Amino acid sequence of fusion protein containing
 ; OTHER INFORMATION: HGE-3 and HGE-1 antigens
 ; US-09-798-042-85

Query Match 19.0%; Score 70; DB 10; Length 658;
 Best Local Similarity 29.6%; Pred. No. 3.9; Mismatches 10; Indels 14; Gaps 3;
 Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;

QY 6 CTESQNLCLCGESNVCGDGN-----KCILGSDEKN-QCVTGEGTPKQPSHNDGDF~ 56
 Db 194 CGDGSSSTTTSNTGTVSETGQVFRDPIRATLKEGDSKNWPPTSGNGTPKPVNDNAKAVA 253

QY 57 --- EEEPEE 62
 Db 254 KDLVQBLTPEE 264

RESULT 11
 US-09-798-042-93
 Sequence 93, Application US/09798042
 ; Patent No. US2002068343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 ; FILE REFERENCE: 210121.439C7
 ; CURRENT APPLICATION NUMBER: US/09/798, 042
 ; CURRENT FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 93
 ; LENGTH: 658
 ; TYPE: PRT

Query Match 19.0%; Score 70; DB 10; Length 658;
 Best Local Similarity 29.6%; Pred. No. 3.9; Mismatches 10; Indels 14; Gaps 3;
 Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;

QY 6 CTESQNLCLCGESNVCGDGN-----KCILGSDEKN-QCVTGEGTPKQPSHNDGDF~ 56
 Db 194 CGDGSSSTTTSNTGTVSETGQVFRDPIRATLKEGDSKNWPPTSGNGTPKPVNDNAKAVA 253

QY 57 --- EEEPEE 62
 Db 254 KDLVQBLTPEE 264

RESULT 12
 US-09-808-602-65
 ; Sequence 65, Application US/09808602
 ; Patent No. US2002015515A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Verne, Corine A
 ; APPLICANT: Fernandes, Elma
 ; APPLICANT: Shimizu, Richard A
 ; APPLICANT: Herrman, John L
 ; APPLICANT: Majundar, Kumud
 ; APPLICANT: Mishra, Vishnu
 ; APPLICANT: MacDougall, John
 ; TITLE OF INVENTION: No. US2002015515A1el Proteins and Nucleic Acids Encoding Same
 ; CURRENT APPLICATION NUMBER: US/09/808, 602
 ; CURRENT FILING DATE: 2001-03-14
 ; PRIORITY NUMBER: 09/800, 198
 ; PRIOR FILING DATE: 2001-03-05
 ; PRIOR APPLICATION NUMBER: 60/186, 596
 ; PRIOR FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 65
 ; LENGTH: 315
 ; TYPE: PRT
 ; ORGANISM: Gallus gallus
 ; US-09-808-602-65

Query Match 18.8%; Score 69; DB 9; Length 315;
 Best Local Similarity 33.3%; Pred. No. 2.3; Mismatches 6; Indels 10; Gaps 3;
 Matches 21; Conservative 6; Mismatches 26; Indels 10; Gaps 3;

QY 7 TESQNLCLC-----EGSNVCGQGNKNCIIG-SDGEEKNOCVTGEGTPKQPSHNDGDFERI 59
 Db 45 TEKGSPPTCLIEQCKPHGRVCGSNGKTYLNHCELHRDACLITGS--KIQQVDGHCKE 101

QY 60 PEE 62
 Db 102 KSE 104

RESULT 13
 US-09-855-722-7
 ; Sequence 7, Application US/09855722
 ; Patent No. US2002049306A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sakano, Seiji
 ; APPLICANT: Itoh, Akira
 ; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
 ; FILE REFERENCE: KP-8576
 ; CURRENT APPLICATION NUMBER: US/09/855, 722
 ; CURRENT FILING DATE: 2001-05-16
 ; PRIORITY NUMBER: 09/214, 278
 ; PRIOR FILING DATE: 1999-01-26
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 7
 ; LENGTH: 1218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-855-722-7

Query Match 18.6%; Score 68.5%; DB 10; Length 1218;
 Best Local Similarity 28.6%; Pred. No. 11; Mismatches 5; Indels 29; Gaps 4;
 Matches 23; Conservative 23; Mismatches 23; Indels 29; Gaps 4;

QY 6 CTESQNLCLCGES-----KCILGSDEKN-QCVTGEGTPKQPSHNDGDF~ 56
 Db 194 CGDGSSSTTTSNTGTVSETGQVFRDPIRATLKEGDSKNWPPTSGNGTPKPVNDNAKAVA 253

QY 57 --- EEEPEE 62
 Db 276 CNPQQ---CLCETNWGGQLDKDINCYGPHQPCINGGTCNSTGPDKYOCSCPCEGSGNS 333

RESULT 14
US-09-976-165-34
; Sequence 34, Application US/09976165
; Patent No. US20020107383A1
GENERAL INFORMATION:
APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASATO
TITLE OF INVENTION: AN ISOLATED NUCLEAR ACID MOLECULE ENCODING HUMAN
FILE REFERENCE: Q-53599
CURRENT APPLICATION NUMBER: US/09/976,165
CURRENT FILING DATE: 2001-10-15
PRIORITY APPLICATION NUMBER: 09/565,538
PRIORITY FILING DATE: 2000-05-05
PRIORITY APPLICATION NUMBER: 09/055,699
PRIORITY FILING DATE: 1998-04-07
PRIORITY APPLICATION NUMBER: 08/820,170
PRIORITY FILING DATE: 1997-03-19
PRIORITY APPLICATION NUMBER: JP 63410/1996
PRIORITY FILING DATE: 1996-03-19
PRIORITY APPLICATION NUMBER: JP 69163/1997
PRIORITY FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 810
TYPE: PRT
ORGANISM: Homo sapiens

RESULT 15
US-10-040-916-6
; Sequence 6, Application US/10040916
; Patent No. US2002014676A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
McCoy, John
LaVallie, Edward
Racie, Lisa
Merberg, David
Treacy, Maurice
Evans, Cheryl
Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

SEARCH RESULTS
Query Match 18.1%; Score 66.5; DB 10; Length 810;
Best Local Similarity 34.4%; Pred. No. 12; Mismatches 9; Indels 7; Gaps 3;
Matches 14; Conservative 7; Mismatches 9; Indels 7; Gaps 3;

Qy 5 DCTESG---ONLC--LCEESNVCGGNKCTIGSDGEKNOC 39
Db 372 NCSEKRHILPENQCCRCRGINFCARGPK---GENSEC 407

Search completed: December 30, 2002, 16:21:06
Job time : 10 secs

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,916
FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/887,029
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: 08/686,878
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
STRANDNESS: <Unknown>
TOPOLogy: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-040-916-6

Query Match 17.9%; Score 66; DB 12; Length 197;
Best Local Similarity 33.3%; Pred. No. 2; 9; Mismatches 6; Indels 8; Gaps 3;
Matches 18; Conservative 6; Mismatches 22; Indels 8; Gaps 3;

Qy 1 LNYTDTESGONLCICEGSNVCGQGNKCLGSDGEKN-----QCVTGECTPKP 40
Db 38 VnSTGTEDGEQPASCTGSEXCXEG--FAISSESEENGESAMDSTVAKEGINVP 8

